

Application No.: Not yet known
Preliminary Amendment dated August 19, 2004

AMENDMENTS TO THE CLAIMS

Listing of Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1 (original): A method of analysing a nucleic acid sample obtained from a site comprising the step of pretreating the sample to remove or inactivate contaminating nucleic acids originating from the site.

Claim 2 (original): A method according to claim 1 wherein the contaminating nucleic acid is deoxyribonucleic acid (DNA), ribonucleic acid (RNA), locked nucleic acid (LNA) or protein nucleic acid (PNA).

Claim 3 (currently amended): A method according to claim 1 ~~or 2~~ wherein the contaminating nucleic acid is particularly well adapted for amplification via PCR or some other amplification process.

Claim 4 (original): A method according to claim 3 wherein the contaminating nucleic acid is an amplicon derived from a PCR or another DNA amplification process.

Claim 5 (currently amended): A method according to ~~any one of claims 1 to 4~~ claim 1 wherein the contaminating nucleic acid is degradation resistant.

Claim 6 (currently amended): A method according to ~~any one of claims 1 to 5~~ claim 1 wherein the contaminating nucleic acid is synthetic.

Claim 7 (currently amended): A method according to ~~any one of claims 1 to 6~~ claim 1 wherein

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the pre- treatment comprises treating the sample to preferentially remove or inactivate nucleic acids that are free or substantially free from other cell components.

Claim 8 (original): A method according to claim 7 wherein the pre-treatment is one or more treatments selected from the group comprising: (i) enzymic treatments; (ii) physical treatments; and (iii) chemical treatments.

Claim 9 (original): A method according to claim 8 wherein the enzymic treatments comprise contacting the sample with DNAses, RNAses, exonucleases and/or 25 endonucleases.

Claim 10 (currently amended): A method according to claim 8 wherein the physical treatments comprise centrifugation, washing, filtration and/or chromatography such as gel filtration chromatography.

Claim 11 (original): A method according to claim 8 wherein the chemical treatments comprise the use of sodium hydroxide, sodium hypochlorite, sodium metabisulphite or ammonium metabisulphite, detergents and/or proprietary products designed to remove nucleic acids from surfaces.

Claim 12 (currently amended): A method ~~of analysing a nucleic acid sample obtained from a site comprising the pre-treatment step of contacting the sample with a nucleic acid probe that 10 preferentially binds to the contaminating nucleic acids and renders them removable from the sample~~ according to claim 1 wherein the method of analysing the nucleic acid sample is PCR, mitochondrial DNA sequencing, single nucleotide polymorphism (SNP) analysis and low copy number PCR.

Claim 13 (currently amended): A method according to claim ~~12~~ 1 wherein the ~~probes is adapted~~

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~~to hybridise to the amplification product of a positive control from a proprietary nucleic acid amplification kit~~ pre-treatment comprises removing cell bound contaminating nucleic acids from the sample.

Claim 14 (currently amended): A method according to claim ~~12 or~~ 13 wherein the ~~nucleic acid probe is labelled~~ cell bound contaminating nucleic acid is particularly well adapted for amplification via PCR or some other amplification process.

Claim 15 (currently amended): A method according to claim ~~14~~ 13 wherein the ~~label is biotin/streptavidin~~ contaminating nucleic acid is of bacterial origin.

Claim 16 (currently amended): A method according to ~~any one of claims 12 to 15~~ further comprising the step of removing the contaminating nucleic acid - probe complex from the sample claim 15 wherein the contaminating nucleic acid is bacteria engineered to contain at least one multicopy plasmid comprising at least one amplicon.

Claim 17 (currently amended): A method according to claim ~~16 wherein the complex is removed using chromatography~~ 13 wherein the cell bound contaminating nucleic acid is removed by exposing the nucleic acid in the cells and then removing the nucleic acid.

Claim 18 (currently amended): A method according to ~~any one of claims 1 to 17~~ wherein the method of analysing the nucleic acid sample is PCR, mitochondrial DNA sequencing, single nucleotide polymorphism (SNP) analysis and low copy number PCR claim 17 wherein the nucleic acid is exposed by lysing the cells.

Claim 19 (currently amended): A method according to claim ~~1~~ wherein the pre-treatment comprises removing cell bound contaminating nucleic acids from the sample 17 wherein the

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nucleic acid is removed using the pre-treatment steps of claim 7.

Claim 20 (currently amended): ~~A method according to claim 19 wherein the cell bound contaminating nucleic acid is particularly well adapted for amplification via PCR or some other amplification process~~ A nucleic acid analysis kit comprising a means to remove a nucleic acid contaminant from a sample to be subjected to analysis.

Claim 21 (currently amended): ~~A method according to claim 19 or 20 wherein the contaminating nucleic acid is of bacterial origin~~ A kit according to claim 20 wherein said means comprises a labelled probe adapted to bind to the contaminant and thus aid in its removal.

Claim 22 (currently amended): ~~A method according to claim 21 wherein the contaminating nucleic acid is bacteria engineered to contain at least one multicopy plasmid comprising at least one amplicon~~ A kit according to claim 20 wherein said means comprises an enzyme or chemical that can be added to the sample and inactivate or remove the contaminant preferentially or selectively relative to a target nucleic acid.

Claims 23-42 (cancelled)